P.50

Endogenous banana streak virus sequences (eBSV) are likely transcriptionally silenced in the resistant seedy diploid Musa balbisiana Pisang Klutuk Wulung (PKW)

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The B genome of banana (*Musa* sp.) harbours integrations of *Banana streak virus* (eBSV) for at least three BSV species, whereas this badnavirus does not require integration for the replication of its ds DNA genome. Some are infectious by releasing a functional viral genome following stresses such as those existing in *in vitro* culture and interspecific crosses contexts. The structure of these eBSV is much longer than a single BSV genome, composed of viral fragments duplicated, more or less extensively rearranged containing at least one full length viral genome.
Wild *M. balbisiana* diploid genotypes (BB) such as Pisang Klutuk Wulung (PKW) harbour such infectious eBSV belonging to three widespread species of BSV (*Goldfinger* -BSGFV, *Imové* – BSIMV and *Obino l'Ewai* - BSOLV) but are nevertheless resistant to any multiplication of BSV without any visible virus particles. Using deep sequencing of total siRNAs of PKW we underlined the presence of virus-derived small RNA (vsRNA) from eBSOLV, eBSGFV and eBSIMV by blasting sequences against the 3 BSV species genomes. Interestingly, we showed that hot and cold spots of vsRNA generation do not target similar viral sequences from one eBSV species to the other but are directly correlated with the structure of the integration. vsRNA are enriched in 24-nt class which represent about 75% of the total 21-24nt siRNA matching eBSV. We also demonstrated that eBSV are highly methylated in the three different sequence contexts (CG, CHH and CHG) throughout the whole sequence of eBSVs with no difference in methylation profile between siRNA producing and non producing areas. Interestingly, methylation patterns of all three eBSV are similar whereas they are located in different genomic context; eBSOLV being in a TE rich area whereas eBSIMV and eBSGFV are in genes rich region. It seems that eBSV are controlled mainly by epigenetic mechanisms similar to those described for transposable elements (TE). All together, our data indicate that eBSVs in PKW genome are likely silenced at the transcriptional level and this is probably responsible for the natural resistance of this genotype to the activation of such infectious eBSV as well as infection by external BSV particles.

Mots-clés : Banana, endogenous banana streak virus (eBSV), methylation, epigenetic.